

Db 593 TACATAAATGATAAATCTTGAGACTAGAGCCAACTGAAATTTTAAGTAATAAACTA 534
QY 80 CAGCGAAAGTCTTCAACAATACGCTAACGACAACGGTGTGACGGTGAATGGACTTACG 139
Db 533 AAGAGAAAACCTATAAGAACAAAGGATTGGTACAAAGTCCATGTGGTGGTGGAATAATC 474
QY 140 ACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCATCA 182
Db 473 ATGGTTTACTAGCAGCTCTATAGTAAATAATCATAATTATTA 431

RESULT 2
BE921962 348 bp mRNA linear EST 07-MAR-2003
LOCUS EST425731 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION cSTB17K20 5' sequence, mRNA sequence.
ACCESSION BE921962
VERSION BE921962.1 GI:10448038
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 348)
AUTHORS van der Hoeven,R.S., Bezzerides,J., Holt,I.E., Liang,F., Cho,J.,
Utterback,T., Hansen,C.L., Doan,B., Bougri,O., Buell,C.R.,
Ronning,C.M., Fry,W.E., Tanksley,S.D. and Baker,B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/.

FEATURES
source
1. .348
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB17K20"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/clone_lib="potato leaves and petioles"
/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

ORIGIN
Query Match 20.0%; Score 39; DB 2; Length 348;
Best Local Similarity 50.8%; Pred. No. 0.6;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 11 ACAATTAATCCTTAATGGTAAACATTTGAAAGCGCGAACAACACTACTGAAGCTGTTGATG 70
Db 124 AAAAAAAAAATGCTGGAAAGTTCGTGTTTGTGGAGATAACAGTTACTGTGTGCGCGTCG 183
QY 71 CTGCTACTGCAGCGAAAGTCTTCAACAATAACGCTAACGACAACGGTGTGACGGTGAAT 130
Db 184 CCGCGCCGATGGTGAAGCGCGGAGCTGAAGAATGACGCGAGCGGTGTGGCGGTGGTG 243
QY 131 GGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCATCATCACTAAG 190
Db 244 GTGGTTCAGAGGAAGAAGATAAGAAATTTTCAGTTGGAATCGTTGGCCACATGAGAAA 303

QY 191 CTT 193
Db 304 CTT 306
RESULT 3
CK249831 925 bp mRNA linear EST 30-JUL-2004
LOCUS EST733468 potato callus cDNA library, normalized and full-length
DEFINITION Solanum tuberosum cDNA clone POCBB33 5' end, mRNA sequence.
ACCESSION CK249831
VERSION CK249831.1 GI:39801339
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 925)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
TITLE Generation of ESTs from potato callus tissue
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST733469
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: Art TAG GTG ACA CTA TAG.
FEATURES
Location/Qualifiers
1. .925
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCBB33"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 20.0%; Score 39; DB 7; Length 925;
Best Local Similarity 50.8%; Pred. No. 0.71;
Matches 93; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 11 ACAATTAATCCTTAATGGTAAACATTTGAAAGCGCGAACAACACTACTGAAGCTGTTGATG 70
Db 170 AAAAAAAAAATGCTGGAAAGTTCGTGTTTGTGGAGATAACAGTTACTGTGTCGCCGTCG 229
QY 71 CTGCTACTGCAGCGAAAGTCTTCAACAATAACGCTAACGACAACGGTGTGACGGTGAAT 130
Db 230 CCGCGCCGATGGTGAAGCGCGGAGCTGAAGAATGACGCGCGGTGTTGGCGGTGGTG 289
QY 131 GGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCATCATCACTAAG 190
Db 290 GTGGTTCAGAGGAAGAAGATAAGAAATTTTTCAGTTGGAATCGTTGGCCACATGAGAAA 349
QY 191 CTT 193
Db 350 CTT 352

RESULT 4
CF434974 652 bp mRNA linear EST 04-SEP-2003
LOCUS EST671319 normalized cDNA library of onion Allium cepa clone
DEFINITION ACABP64, mRNA sequence.
ACCESSION CF434974

Db	111	ACGATGACGACGACGATGATGAAGAAGAGGAGGGTGATGGTGCAGAACAAAGATGATG	52
QY	161	CAGTTACTGAACATCACCATCACTAA	189
Db	51	AAGATAATGAACAACAACAACAACAA	23
RESULT 11			
CD084228			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
QY	41	AAGCGAACAACTACTGAAGCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAAT	100
Db	163	AAGTAGGACGAGGTGATGGAGATGATGATGGAGATGAAGATGATGTCGATGATG	222
QY	101	ACGCTAACGACAACGGTGTGACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTA	160
Db	223	ACGATGACGACGACGATGATGAAGAAGAGGAGGGTGGTGGTGCAGACAAGATGATG	282
QY	161	CAGTTACTGAACATCACCATCACTAA	189

Db	283	AAGATAATGAACAACAACAACAACAA	311
RESULT 12			
AZ166486			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
QY	49	ACAACTACTGAAGCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAAC	108
Db	359	ACTACTACCAATACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT	418
QY	109	GACAAACGGTGTGACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACT	168
Db	419	TACTACAGNGACAATGATCCATCTAATTATGACTCTTATTACTACTATAATAAATTACTACT	478
QY	169	GAACATCACCATCATCACTA	188
Db	479	ACCTAATACTACTACTACTA	498
RESULT 13			
AJ599051/c			
LOCUS			
DEFINITION			
ACCESSION			


```
VERSION      AJ599051.1 GI:37948679
KEYWORDS     GSS; right border; T-DNA flanking sequence.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
REFERENCE    1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
              of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE      22363535
PUBMED       12446565
REFERENCE    2 (bases 1 to 869)
AUTHORS      Balzergue,S.
TITLE        Direct Submission
JOURNAL      Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
COMMENT      Gaston Cremieux, 91057 Evry cedex, FRANCE
              PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).
FEATURES     Location/Qualifiers
              1..869
               /organism="Arabidopsis thaliana"
               /mol_type="genomic DNA"
               /cultivar="Wassillewskija"
               /db_xref="taxon:3702"
               /clone="479E08"
               /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              misc_feature 1:..869
               /note="T-DNA flanking sequence
               right border"
ORIGIN
Query Match      18.8%; Score 36.6; DB 9; Length 869;
Best Local Similarity 57.4%; Pred. No. 3.8;
Matches 66; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 51 AACTACTGAAGCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGA 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 645 ATCTCTTGAATCGGAAGAAGCTTCTTCGTCGCGAAAGCAATCGAAGAAGCTTACGC 586
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 111 CAACGGTGTGACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTT 165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 585 CGTCGCTTCTGCCACCCTATTTCGGTGATGACGACGGGATCGAGATTCTTAAAGCT 531

RESULT 14
CNS07C24/c LOCUS
DEFINITION T7 end of clone BD0AA008B01 of library BD0AA from strain CBS 94 of
            Candida tropicalis, genomic survey sequence.
ACCESSION  AL439814
VERSION     AL439814.1 GI:12232226
KEYWORDS    GSS.
SOURCE      Candida tropicalis
ORGANISM    Candida tropicalis
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; mitosporic Saccharomycetales; Candida.
REFERENCE   1 (bases 1 to 888)
AUTHORS     Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
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de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
MEDLINE     11152876
PUBMED      11152876
REFERENCE    2 (bases 1 to 888)
AUTHORS      Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
            Dujon,B.
TITLE        Genomic exploration of the hemiascomycetous yeasts: 16. Candida
            tropicalis
JOURNAL      FEBS Lett. 487 (1), 91-94 (2000)
MEDLINE      20584726
PUBMED       11152891
REFERENCE    3 (bases 1 to 888)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web :
            This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES     Location/Qualifiers
              1..888
               /organism="Candida tropicalis"
               /mol_type="genomic DNA"
               /strain="CBS 94"
               /db_xref="taxon:5482"
               /clone="BD0AA008B01"
               /clone_lib="BD0AA"
               /note="end : T7"
ORIGIN
Query Match      18.7%; Score 36.4; DB 9; Length 888;
Best Local Similarity 56.8%; Pred. No. 4.3;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 46 GAAACAACACTGAAGCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCT 105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 650 GAAGAAACCCAGGAGCTGCTGAACCCACCCTGCTGCTGAAGAAACCCAGGAGCGCT 591
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 106 AACGACAACGGTGTGACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAG 163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 GAAACCACCACCTGCTGCTGAAGAAACCACTGAAGCCGCTGAACCAACCACCACTGCTGCTG 533

RESULT 15
CD534749/c LOCUS
DEFINITION 40N18 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
            3', mRNA sequence.
ACCESSION  CD534749
VERSION     CD534749.1 GI:40454761
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 411)
AUTHORS     Guo,Y., Cai,Z. and Gan,S.
TITLE       Transcriptome of Arabidopsis leaf senescence
```

```

FEATURES
source
Location/Qualifiers
1. .411
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecot_type="Landsberg erecta"
/db_xref="taxon:3702"
/tissue_type="Leaf"
/dev_stage="Yellow Leaf With Greenish Base Area"
/lab_host="E. coli"
/clone_lib="Arabidopsis Leaf Senescence Library"
/note="Organ: Rosette Leaf; Vector: pBluscript SKII+;
Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5
and #6 (counted from the bottom) were harvested and
immediately frozen in liquid N2. The leaves were visibly
yellow excepted for the leaf base areas that were still
greenish."

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```

Query Match          18.5%; Score 36; DB 6; Length 411;
Best Local Similarity 58.3%; Pred. No. 5;
Matches 63; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

```

112 AACGGTGTGACGGTGAATGGACTTACGACGATCGGACTAGACCTTT 159
334 GTTGTCTTCGAATGCTGTGTCGAGTGTGATGATGGGATTAAGATTCTT 287

Search completed: August 10, 2005, 23:51:00
Job time : 3106 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2005, 13:36:38 ; Search time 430 Seconds
(without alignments)
2684.534 Million cell updates/sec

Title: US-10-672-108-5
Perfect score: 195
Sequence: 1 atgactactacaaattaat.....accatcatcactaagcttga 195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues 8780412

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	100.0	195	4 AAC86821	Aac86821 Nucleotid
2	191.8	98.4	195	4 AAC86827	Aac86827 Nucleotid
3	191.8	98.4	195	4 AAC86820	Aac86820 Nucleotid
4	190.2	97.5	195	4 AAC86828	Aac86828 Nucleotid
5	190.2	97.5	195	4 AAC86829	Aac86829 Nucleotid
6	188.6	96.7	195	4 AAC86825	Aac86825 Nucleotid
7	187	95.9	195	4 AAC86822	Aac86822 Nucleotid
8	187	95.9	195	4 AAC86823	Aac86823 Nucleotid
9	187	95.9	195	4 AAC86824	Aac86824 Nucleotid
10	183.8	94.3	195	4 AAC86826	Aac86826 Nucleotid
11	163.8	84.0	1308	2 AAQ50453	Aaq50453 Sequence
12	162.6	83.4	396	1 AAN94677	Aan94677 Protein G
13	162.6	83.4	396	2 AAQ06013	Aaq06013 Sequence
14	162.6	83.4	396	2 AAQ64749	Aaq64749 IGG-bind
15	162.6	83.4	435	1 AAN91100	Aan91100 Protein G
16	162.6	83.4	435	2 AAQ06008	Aaq06008 Sequence
17	162.6	83.4	435	2 AAQ10005	Aaq10005 Type 3 GX
18	162.6	83.4	435	2 AAQ64647	Aaq64647 IGG-bind
19	162.6	83.4	447	1 AAN91103	Aan91103 Protein G
20	162.6	83.4	447	2 AAQ06006	Aaq06006 Sequence

21	162.6	83.4	447	2 AAQ10004	Aaq10004 Type 1 St
22	162.6	83.4	447	2 AAQ64645	Aaq64645 IGG-bind
23	162.6	83.4	495	1 AAN91108	Aan91108 Protein G
24	162.6	83.4	495	2 AAQ06016	Aaq06016 Sequence
25	162.6	83.4	495	2 AAQ10011	Aaq10011 Type 9 GX
26	162.6	83.4	495	2 AAQ64748	Aaq64748 IGG-bind
27	162.6	83.4	600	1 AAN91104	Aan91104 Protein G
28	162.6	83.4	600	2 AAQ06007	Aaq06007 Sequence
29	162.6	83.4	600	2 AAQ10003	Aaq10003 Type 2 GX
30	162.6	83.4	600	2 AAQ64646	Aaq64646 IGG-bind
31	162.6	83.4	606	2 AAQ10009	Aaq10009 Type 8 GX
32	162.6	83.4	750	2 AAQ10008	Aaq10008 Type 6 GX
33	162.6	83.4	798	1 AAN91099	Aan91099 Protein G
34	162.6	83.4	798	2 AAQ06009	Aaq06009 Sequence
35	162.6	83.4	798	2 AAQ10007	Aaq10007 Type 4 GX
36	162.6	83.4	798	2 AAQ64648	Aaq64648 IGG-bind
37	162.6	83.4	810	1 AAN94674	Aan94674 Protein G
38	162.6	83.4	810	2 AAQ06011	Aaq06011 Sequence
39	162.6	83.4	810	2 AAQ64649	Aaq64649 IGG-bind
40	162.6	83.4	1469	1 AAN70757	Aan70757 Sequence
41	162.6	83.4	1949	2 AAQ06018	Aaq06018 Sequence
42	162.6	83.4	1950	1 AAN91093	Aan91093 Protein G
43	162.6	83.4	1950	1 AAN91094	Aan91094 Protein G
44	162.6	83.4	1950	2 AAQ06017	Aaq06017 Sequence
45	162.6	83.4	1950	2 AAQ10001	Aaq10001 Sequecne

ALIGNMENTS

RESULT 1
AAC86821
ID AAC86821 standard; DNA; 195 BP.
XX
AC AAC86821;
XX
DT 02-APR-2001 (first entry)
XX
DE Nucleotide sequence of a B1 domain of protein G with mutation E27A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.
XX
OS Synthetic.
OS Streptococcus sp.
XX
FH Key Location/Qualifiers
CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR P-PSDB; AAB30886.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an Igg but does not bind Fc fragment.
XX
PS Claim 34; Page 73; 83pp; English.

XX The present sequence encodes a mutated B1 domain of the bacterial protein
CC G. The B1 domain exhibits binding activity for a Fab fragment of an
CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
CC of an IgG. The B1 domain may further comprise a disrupted or mutated
CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
CC residue of the mature B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity
CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample

XX Sequence 195 BP; 68 A; 42 C; 37 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 195; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 9e-47;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGAAACAACACTACTGAA 60
Db |||||
1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTACTGCAGCGAAAGTCTTCAACAATACGCTAACGACAACGGTGT 120
Db |||||
61 GCTGTTGATGCTACTGCAGCGAAAGTCTTCAACAATACGCTAACGACAACGGTGT 120
QY 121 GACGGTGAATGGACTTACGACGATCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db |||||
121 GACGGTGAATGGACTTACGACGATCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTGA 195
Db |||||
181 CATCACTAAGCTTGA 195

RESULT 2

AAC86827
ID AAC86827 standard; DNA; 195 BP.
XX
AC AAC86827;
XX
DT 02-APR-2001 (first entry)
XX
DE Nucleotide sequence of a mutated B1 domain of protein G.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.
XX
OS Synthetic.
OS Streptococcus sp.

Key Location/Qualifiers
FH CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c

XX WO200074728-A1.
XX
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX WPI; 2001-049994/06.

DR P-PSDB; AAB30894.

XX B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 34; Page 78-79; 83pp; English.
XX

CC The present sequence encodes a mutated B1 domain of the bacterial protein
CC G. The B1 domain exhibits binding activity for a Fab fragment of an
CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
CC of an IgG. The B1 domain may further comprise a disrupted or mutated
CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
CC residue of the mature B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity
CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample

XX Sequence 195 BP; 68 A; 41 C; 36 G; 50 T; 0 U; 0 Other;

Query Match 98.4%; Score 191.8; DB 4; Length 195;
Best Local Similarity 99.0%; Pred. No. 7.7e-46;
Matches 193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db |||||
1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTACTGCAGCGAAAGTCTTCAACAATACGCTAACGACAACGGTGT 120
Db |||||
61 GCTGTTGATGCTACTGCAGTTAAAGTCTTCAACAATACGCTAACGACAACGGTGT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db |||||
121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTGA 195
Db |||||
181 CATCACTAAGCTTGA 195

RESULT 3

AAC86820
ID AAC86820 standard; DNA; 195 BP.
XX
AC AAC86820;
XX
DT 02-APR-2001 (first entry)
XX
DE Nucleotide sequence of the native B1 domain of protein G.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.

XX Streptococcus sp.

Key Location/Qualifiers
FH CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c

XX WO200074728-A1.
XX
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.

XX PA (UYDU-) UNIV DUKE.

XX PI Hellinga HW, Sloan DJ;

XX XX

DR WPI; 2001-049994/06.

DR P-PSDB; AAB30883.

XX B1 domain polypeptide of bacterial protein G, useful for detection and

PT purification of antibody fragments, exhibits binding activity for Fab

PT fragment of an IgG but does not bind Fc fragment.

XX

PS Disclosure; Page 50; 83pp; English.

XX

CC The present sequence encodes a native B1 domain of the bacterial protein

CC G. The B1 domain exhibits binding activity for a Fab fragment of an

CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment

CC of an IgG. The B1 domain may further comprise a disrupted or mutated

CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27

CC residue of the mature B1 domain acts as a charged knob on the surface of

CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of

CC this residue virtually abolishes stable complex formation. The B1 domain

CC can be immobilized to a solid phase support, and be used for purifying Fc

CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity

CC chromatography. The B1 domain is also useful for detecting IgG or its

CC fragments in a clinical sample

XX

SQ Sequence 195 BP; 70 A; 41 C; 36 G; 48 T; 0 U; 0 Other;

Query Match 98.4%; Score 191.8; DB 4; Length 195;

Best Local Similarity 99.0%; Pred. No. 7.7e-46;

Matches 193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60

Db 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60

QY 61 GCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120

Db 61 GCTGTTGATGCTGCTACTGCAGAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120

QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY 181 CATCACTAAGCTTGA 195

Db 181 CATCACTAAGCTTGA 195

RESULT 4

AAC86828

ID AAC86828 standard; DNA; 195 BP.

XX

AC AAC86828;

XX

DT 02-APR-2001 (first entry)

XX

DE Nucleotide sequence of a mutated B1 domain of protein G.

XX

KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;

KW knobs-into-holes binding site; ss.

XX

OS Synthetic.

OS Streptococcus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..189

FT /*tag= a

FT /product= "B1 domain of protein G"

FT mat_peptide 4..189

FT /*tag= c

XX

PN WO200074728-A1.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-US015366.

XX

PR 04-JUN-1999; 99US-00326342.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Hellinga HW, Sloan DJ;

XX

DR WPI; 2001-049994/06.

DR P-PSDB; AAB30925.

XX

PT B1 domain polypeptide of bacterial protein G, useful for detection and

PT purification of antibody fragments, exhibits binding activity for Fab

PT fragment of an IgG but does not bind Fc fragment.

XX

PS Claim 34; Page 79; 83pp; English.

XX

CC The present sequence encodes a mutated B1 domain of the bacterial protein

CC G. The B1 domain exhibits binding activity for a Fab fragment of an

CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment

CC of an IgG. The B1 domain may further comprise a disrupted or mutated

CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27

CC residue of the mature B1 domain acts as a charged knob on the surface of

CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of

CC this residue virtually abolishes stable complex formation. The B1 domain

CC can be immobilized to a solid phase support, and be used for purifying Fc

CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity

CC chromatography. The B1 domain is also useful for detecting IgG or its

CC fragments in a clinical sample

XX

SQ Sequence 195 BP; 69 A; 41 C; 35 G; 50 T; 0 U; 0 Other;

Query Match 97.5%; Score 190.2; DB 4; Length 195;

Best Local Similarity 98.5%; Pred. No. 2.2e-45;

Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60

Db 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60

QY 61 GCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120

Db 61 GCTGTTGATGCTGCTACTGCATTAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120

QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY 181 CATCACTAAGCTTGA 195

Db 181 CATCACTAAGCTTGA 195

RESULT 5

AAC86829

ID AAC86829 standard; DNA; 195 BP.

XX

AC AAC86829;

XX

DT 02-APR-2001 (first entry)

XX

DE Nucleotide sequence of a mutated B1 domain of protein G.

XX

KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;

KW knobs-into-holes binding site; ss.

XX

OS Synthetic.

OS Streptococcus sp.

XX

```

FH Key          Location/Qualifiers
FT CDS          1..189
FT              /*tag= a
FT              /product= "B1 domain of protein G"
FT mat_peptide  4..189
FT              /*tag= c
XX
XX WO200074728-A1.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-US015366.
XX
XX 04-JUN-1999; 99US-00326342.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Hellinga HW, Sloan DJ;
XX
XX WPI; 2001-049994/06.
XX P-PSDB; AAB30926.
XX
XX B1 domain polypeptide of bacterial protein G, useful for detection and
XX purification of antibody fragments, exhibits binding activity for Fab
XX fragment of an IgG but does not bind Fc fragment.
XX
XX Claim 34; Page 80; 83pp; English.
XX
XX The present sequence encodes a mutated B1 domain of the bacterial protein
XX G. The B1 domain exhibits binding activity for a Fab fragment of an
XX immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
XX of an IgG. The B1 domain may further comprise a disrupted or mutated
XX "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
XX residue of the mature B1 domain acts as a charged knob on the surface of
XX the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
XX this residue virtually abolishes stable complex formation. The B1 domain
XX can be immobilized to a solid phase support, and be used for purifying Fc
XX and Fab fragments of IgG from a warm-blooded vertebrate by affinity
XX chromatography. The B1 domain is also useful for detecting IgG or its
XX fragments in a clinical sample
XX
XX Sequence 195 BP; 69 A; 41 C; 35 G; 50 T; 0 U; 0 Other;
XX
XX Query Match          97.5%; Score 190.2; DB 4; Length 195;
XX Best Local Similarity 98.5%; Pred. No. 2.2e-45;
XX Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 ATGACTACTTACAAATTAATCCTTAATGGTTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTAATCCTTAATGGTTAAACATTGAAAGCGGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTACTGCGAGCGAAAGTCTTCAAAACAATACGCTAACGACAACGGTGTT 120
Db 61 GCTGTTGATGCTACTGCGAATTAAGTCTTCAAAACAATACGCTAACGACAACGGTGTT 120
QY 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTTGA 195
Db 181 CATCACTAAGCTTTGA 195
RESULT 6
AAC86825
ID AAC86825 standard; DNA; 195 BP.
XX
XX AAC86825;
XX
XX 02-APR-2001 (first entry)
XX
XX Nucleotide sequence of a B1 domain of protein G with mutation W43A.
```

```

XX B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
XX knobs-into-holes binding site; ss.
XX
XX Synthetic.
XX Streptococcus sp.
XX
XX Key          Location/Qualifiers
XX CDS          1..189
XX              /*tag= a
XX              /product= "B1 domain of protein G"
XX mat_peptide  4..189
XX              /*tag= c
XX
XX WO200074728-A1.
XX
XX 14-DEC-2000.
XX
XX 02-JUN-2000; 2000WO-US015366.
XX
XX 04-JUN-1999; 99US-00326342.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Hellinga HW, Sloan DJ;
XX
XX WPI; 2001-049994/06.
XX P-PSDB; AAB30892.
XX
XX B1 domain polypeptide of bacterial protein G, useful for detection and
XX purification of antibody fragments, exhibits binding activity for Fab
XX fragment of an IgG but does not bind Fc fragment.
XX
XX Claim 34; Page 77; 83pp; English.
XX
XX The present sequence encodes a mutated B1 domain of the bacterial protein
XX G. The B1 domain exhibits binding activity for a Fab fragment of an
XX immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
XX of an IgG. The B1 domain may further comprise a disrupted or mutated
XX "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
XX residue of the mature B1 domain acts as a charged knob on the surface of
XX the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
XX this residue virtually abolishes stable complex formation. The B1 domain
XX can be immobilized to a solid phase support, and be used for purifying Fc
XX and Fab fragments of IgG from a warm-blooded vertebrate by affinity
XX chromatography. The B1 domain is also useful for detecting IgG or its
XX fragments in a clinical sample
XX
XX Sequence 195 BP; 70 A; 42 C; 36 G; 47 T; 0 U; 0 Other;
XX
XX Query Match          96.7%; Score 188.6; DB 4; Length 195;
XX Best Local Similarity 97.9%; Pred. No. 6.5e-45;
XX Matches 191; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 1 ATGACTACTTACAAATTAATCCTTAATGGTTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTAATCCTTAATGGTTAAACATTGAAAGCGGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTGCTACTGCGAGCGAAAGTCTTCAAAACAATACGCTAACGACAACGGTGTT 120
Db 61 GCTGTTGATGCTGCTACTGCGAGAAAAGTCTTCAAAACAATACGCTAACGACAACGGTGTT 120
QY 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAAGCGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTTGA 195
Db 181 CATCACTAAGCTTTGA 195
RESULT 7
AAC86822
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ID AAC86822 standard; DNA; 195 BP.
XX
AC AAC86822;
XX
DT 02-APR-2001 (first entry)
XX
DE Nucleotide sequence of a B1 domain of protein G with mutation K28A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.
XX
OS Synthetic.
OS Streptococcus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c
XX
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR P-PSDB; AAB30887.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 34; Page 74; 83pp; English.
XX
CC The present sequence encodes a mutated B1 domain of the bacterial protein
CC G. The B1 domain exhibits binding activity for a Fab fragment of an
CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
CC of an IgG. The B1 domain may further comprise a disrupted or mutated
CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
CC residue of the mature B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity
CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample
XX
SQ Sequence 195 BP; 67 A; 42 C; 38 G; 48 T; 0 U; 0 Other;

Query Match 95.9%; Score 187; DB 4; Length 195;
Best Local Similarity 97.4%; Pred. No. 1.9e-44;
Matches 190; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
DB |||||||
1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60

QY 61 GCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACCGGTGTT 120
DB |||||||
61 GCTGTTGATGCTGCTACTGCAGAGCGGTCTTCAAACAATACGCTAACGACAACCGGTGTT 120

QY 121 GACGGTGAATGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
DB |||||||
121 GACGGTGAATGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
```

```
QY 181 CATCACTAAGCTTGA 195
DB |||||||
181 CATCACTAAGCTTGA 195

RESULT 8
AAC86823
ID AAC86823 standard; DNA; 195 BP.
XX
AC AAC86823;
XX
DT 02-APR-2001 (first entry)
XX
DE Nucleotide sequence of a B1 domain of protein G with mutation K31A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.
XX
OS Synthetic.
OS Streptococcus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c
XX
XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR P-PSDB; AAB30888.
XX
PT B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.
XX
PS Claim 34; Page 74-75; 83pp; English.
XX
CC The present sequence encodes a mutated B1 domain of the bacterial protein
CC G. The B1 domain exhibits binding activity for a Fab fragment of an
CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
CC of an IgG. The B1 domain may further comprise a disrupted or mutated
CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
CC residue of the mature B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity
CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample
XX
SQ Sequence 195 BP; 67 A; 42 C; 38 G; 48 T; 0 U; 0 Other;

Query Match 95.9%; Score 187; DB 4; Length 195;
Best Local Similarity 97.4%; Pred. No. 1.9e-44;
Matches 190; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
DB |||||||
1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60

QY 61 GCTGTTGATGCTGCTACTGCTGACGCGAAAGTCTTCAAACAATACGCTAACGACAACCGGTGTT 120
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Db 61 GCTGTTGATGCTGCTACTGCAGAAAAGTCTTCGGCGAATACGCTAACGACAACGGTGT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAAATCACCACAT 180
Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAAATCACCACAT 180
QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195

RESULT 9
AAC86824
ID AAC86824 standard; DNA; 195 BP.
XX
AC AAC86824;
XX
DT 02-APR-2001 (first entry)
XX
DE Nucleotide sequence of a B1 domain of protein G with mutation N35A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.
XX
OS Synthetic.
OS Streptococcus sp.

XX
FH Key Location/Qualifiers
FT CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c

XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.

XX (UYDU-) UNIV DUKE.
XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR P-PSDB; AAB30889.

XX B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.

XX Claim 34; Page 75; 83pp; English.

XX The present sequence encodes a mutated B1 domain of the bacterial protein
CC G. The B1 domain exhibits binding activity for a Fab fragment of an
CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
CC of an IgG. The B1 domain may further comprise a disrupted or mutated
CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
CC residue of the mature B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity
CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample

XX Sequence 195 BP; 68 A; 41 C; 38 G; 48 T; 0 U; 0 Other;

SQ Query Match 95.9%; Score 187; DB 4; Length 195;
Best Local Similarity 97.4%; Pred. No. 1.9e-44;

Matches 190; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTGCTACTGCAGCGAAAAGTCTTCAAAACAATACGCTAACGACAACGGTGT 120
Db 61 GCTGTTGATGCTGCTACTGCAGAAAAGTCTTCAAAACAATACGCTGCGGACAACGGTGT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAAATCACCACAT 180
Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAAATCACCACAT 180
QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195

RESULT 10
AAC86826
ID AAC86826 standard; DNA; 195 BP.

XX AAC86826;

XX
DT 02-APR-2001 (first entry)

XX
DE Nucleotide sequence of a B1 domain of protein G with mutation T44A/Y45A.
XX
KW B1 domain; protein G; Fab fragment; immunoglobulin G; IgG; Fc fragment;
KW knobs-into-holes binding site; ss.

XX
OS Synthetic.
OS Streptococcus sp.

XX
FH Key Location/Qualifiers
FT CDS 1..189
FT /*tag= a
FT /product= "B1 domain of protein G"
FT mat_peptide 4..189
FT /*tag= c

XX
PN WO200074728-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-US015366.
XX
PR 04-JUN-1999; 99US-00326342.

XX (UYDU-) UNIV DUKE.

XX
PI Hellinga HW, Sloan DJ;
XX
DR WPI; 2001-049994/06.
DR P-PSDB; AAB30893.

XX B1 domain polypeptide of bacterial protein G, useful for detection and
PT purification of antibody fragments, exhibits binding activity for Fab
PT fragment of an IgG but does not bind Fc fragment.

XX Claim 34; Page 78; 83pp; English.

XX The present sequence encodes a mutated B1 domain of the bacterial protein
CC G. The B1 domain exhibits binding activity for a Fab fragment of an
CC immunoglobulin (Ig) G but exhibits no binding activity for a Fc fragment
CC of an IgG. The B1 domain may further comprise a disrupted or mutated
CC "knobs-into-holes" binding site for a Fc fragment of an IgG. The Glu27
CC residue of the mature B1 domain acts as a charged knob on the surface of
CC the B1 domain, inserting a polar hole on the Fc fragment. A mutation of
CC this residue virtually abolishes stable complex formation. The B1 domain
CC can be immobilized to a solid phase support, and be used for purifying Fc
CC and Fab fragments of IgG from a warm-blooded vertebrate by affinity

CC chromatography. The B1 domain is also useful for detecting IgG or its
CC fragments in a clinical sample
XX
SQ Sequence 195 BP; 68 A; 41 C; 40 G; 46 T; 0 U; 0 Other;
Query Match 94.3%; Score 183.8; DB 4; Length 195;
Best Local Similarity 96.4%; Pred. No. 1.6e-43;
Matches 188; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120
Db 61 GCTGTTGATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120
QY 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAATGGCGGCGGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195
RESULT 11
AAQ50453
ID AAQ50453 standard; DNA; 1308 BP.
XX
AC AAQ50453;
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-MAY-1994 (first entry)
XX
DE Sequence encoding immunoglobulin light chain binding protein.
XX Immunoglobulin; light chain; binding; identification; purification;
KW separation; ss.
KW Escherichia coli.
OS
XX WO9322342-A1.
PN
XX 11-NOV-1993.
PD
XX 28-APR-1993; 93WO-SE0000375.
PF
XX 28-APR-1992; 92SE-00001331.
PR
XX (HIGH-) HIGHTECH RECEPTOR AB.
PA
XX Bjoerck L, Sjoerbring U;
PI
XX WPI; 1993-368722/46.
DR P-PSDB; AAR42994.
XX
XX New protein L binding light chains of all immunoglobulin classes - for
PT binding purifying and identifying immunoglobulin, also related DNA,
PT vectors and host cells.
XX
PS Claim 6; Page 39-40; 71pp; English.
XX
CC Protein L (AAR42993) is capable of binding to immunoglobulin G light
CC chains. It is useful for binding, separating (purifying) and identifying
CC immunoglobulin and for removing immunoglobulin molecules from serum. This
CC is the coding sequence of one hybrid protein of the L protein. The hybrid
CC proteins can bind all human immunoglobulin classes and many
CC immunoglobulins from other species. They are highly soluble and retain
CC their binding activity at high temperatures over a pH range of 3-10. They
CC can be immobilised without loss of activity. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)

XX
SQ Sequence 1308 BP; 577 A; 204 C; 252 G; 275 T; 0 U; 0 Other;
Query Match 84.0%; Score 163.8; DB 2; Length 1308;
Best Local Similarity 96.0%; Pred. No. 1.7e-37;
Matches 168; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 919 ATGGACACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 978
QY 61 GCTGTTGATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120
Db 979 GCTGTTGATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 1038
QY 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 175
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RESULT 12
AAN94677
ID AAN94677 standard; DNA; 396 BP.
XX
AC AAN94677;
XX
DT 25-MAR-2003 (revised)
DT 04-JUL-1990 (first entry)
XX
DE Protein G gene variant.
XX
KW Protein G; immunoglobulin; Fc receptor; ds.
XX
OS Streptococcus sp.
XX WO8810306-A.
PN
XX 29-DEC-1988.
PD
XX 20-JUN-1988; 88WO-US002084.
PF
XX 19-JUN-1987; 87US-00063959.
PR
XX (GEMX) GENEX CORP.
PA (PHAA) PHARMACIA AB.
XX
PI Fahnstock SR;
XX
XX WPI; 1989-023848/03.
DR P-PSDB; AAP94791.
XX
XX Cloned protein G variant genes - expressing proteins having
PT immunoglobulin-binding properties of protein G and derived from
PT Streptococcus sp.
XX
PS Claim 10; Page 86; 116pp; English.
XX
CC Gene encodes protein G variant of non-pathogenic streptococcus allowing
CC isolation of the protein and variants, useful as bacterial Fc receptors
CC eg in purification and detection of Abs., screening of hybridoma clones
CC and treatment of disease. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 396 BP; 149 A; 87 C; 79 G; 81 T; 0 U; 0 Other;
Query Match 83.4%; Score 162.6; DB 1; Length 396;
Best Local Similarity 97.6%; Pred. No. 2.8e-37;
Matches 165; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 66
Db 31 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 90
QY 67 GATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 126

Db 91 GATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGTGACGGT 150

Qy 127 GAATGGACTTACGACGATGCGACTAAGACCTTTTACAGTTACTGAACATC 175

Db 151 GAATGGACTTACGACGATGCGACTAAGACCTTTTACAGTTACTGAACAAAC 199

RESULT 13

AAQ06013

ID AAQ06013 standard; DNA; 396 BP.

XX

AC AAQ06013;

XX

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 17-JAN-1991 (first entry)

XX

DE Sequence encoding Protein G variant.

XX

KW Immunoglobulin; ds.

XX

OS Streptococcus sp; Lancefield Group G strain.

XX

PN US4956296-A.

XX

PD 11-SEP-1990.

XX

PF 20-JUN-1988; 88US-00209236.

XX

PR 14-FEB-1986; 86US-00829354.

PR 23-APR-1986; 86US-00854887.

PR 17-FEB-1987; 87WO-US000329.

PR 19-JUN-1987; 87US-00063959.

XX

PA (GEMX) GENEX CORP.

XX

PI Fahnestock SR;

XX

DR WPI; 1990-297491/39.

DR P-PSDB; AAR07008.

XX

PT Recombinant Protein G variants - obtd. using a cloned gene encoding Protein G from Streptococcus sp., used for binding immunoglobulin.

XX

PS Claim 8; Col 49; 48pp; English.

XX

CC Sequence may be incorporated into a non-pathogenic host eg. E.coli, where they may be expressed at high levels. The proteins have a higher binding efficiency and capacity for immunoglobulin, and may be used for purifying, detecting and isolating antibodies. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

XX

SQ Sequence 396 BP; 149 A; 87 C; 79 G; 81 T; 0 U; 0 Other;

Query Match 83.4%; Score 162.6; DB 2; Length 396;

Best Local Similarity 97.6%; Pred. No. 2.8e-37;

Matches 165; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAAGCTGTT 66

Db 31 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAAGCTGTT 90

Qy 67 GATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGTGACGGT 126

Db 91 GATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGTGACGGT 150

Qy 127 GAATGGACTTACGACGATGCGACTAAGACCTTTTACAGTTACTGAACATC 175

Db 151 GAATGGACTTACGACGATGCGACTAAGACCTTTTACAGTTACTGAACAAAC 199

AAQ64749

ID AAQ64749 standard; DNA; 396 BP.

XX

AC AAQ64749;

XX

DT 25-MAR-2003 (revised)

DT 06-JAN-1995 (first entry)

XX

DE IgG-binding Streptococcus Protein G variant coding sequence.

XX

KW Streptococcus Protein G; variant; IgG binding activity; immunoglobulin; Lancefield Group G; bacterial Fc receptor; ss.

XX

OS Streptococcus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..396

FT /*tag= a

FT /product= "Protein_G_variant"

XX

PN US5312901-A.

XX

PD 17-MAY-1994.

XX

PF 21-APR-1992; 92US-00871539.

XX

PR 14-FEB-1986; 86US-00829354.

PR 23-APR-1986; 86US-00854887.

PR 19-JUN-1987; 87US-00063959.

PR 20-JUN-1988; 88US-00209236.

PR 19-JUN-1990; 90US-00540169.

XX

PA (PHAA) PHARMACIA LKB BIOTECHNOLOGY AB.

XX

PI Fahnestock SR;

XX

DR WPI; 1994-159179/19.

DR P-PSDB; AAR53300.

XX

PT New recombinant streptococcal protein G variants - useful for antibody detection and purification and for therapy.

PT

PS Disclosure; Col 15 and 16; 48pp; English.

XX

CC Protein G isolated from Streptococcus has IgG-binding activity which has been localised to the B repeating structure (see AAR53290). The nucleotide sequence AAQ64749 codes for a claimed Streptococcal Protein G variant comprising the B domain active site and retaining IgG-binding activity. (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 396 BP; 149 A; 87 C; 79 G; 81 T; 0 U; 0 Other;

Query Match 83.4%; Score 162.6; DB 2; Length 396;

Best Local Similarity 97.6%; Pred. No. 2.8e-37;

Matches 165; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAAGCTGTT 66

Db 31 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAAGCTGTT 90

Qy 67 GATGCTGCTACTGCAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGTGACGGT 126

Db 91 GATGCTGCTACTGCAGAAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGTGACGGT 150

Qy 127 GAATGGACTTACGACGATGCGACTAAGACCTTTTACAGTTACTGAACATC 175

Db 151 GAATGGACTTACGACGATGCGACTAAGACCTTTTACAGTTACTGAACAAAC 199

RESULT 15

AAN91100

ID AAN91100 standard; DNA; 435 BP.

XX

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2005, 15:15:58 ; Search time 1719 Seconds
(without alignments)
5496.665 Million cell updates/sec

Title: US-10-672-108-5
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
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- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	195	6 AR438294	AR438294 Sequence
2	191.8	98.4	195	6 AR438293	AR438293 Sequence
3	191.8	98.4	195	6 AR438300	AR438300 Sequence
4	190.2	97.5	195	6 AR438301	AR438301 Sequence
5	190.2	97.5	195	6 AR438302	AR438302 Sequence
6	188.6	96.7	195	6 AR438298	AR438298 Sequence
7	187	95.9	195	6 AR438295	AR438295 Sequence
8	187	95.9	195	6 AR438296	AR438296 Sequence
9	187	95.9	195	6 AR438297	AR438297 Sequence
10	183.8	94.3	195	6 AR438299	AR438299 Sequence
11	163.8	84.0	1308	6 AR079001	AR079001 Sequence
12	163.8	84.0	1365	1 S50809	S50809 protein LG=
13	162.6	83.4	396	6 I09113	I09113 Sequence 10
14	162.6	83.4	435	6 I09106	I09106 Sequence 3
15	162.6	83.4	447	6 I09104	I09104 Sequence 1
16	162.6	83.4	495	6 I09112	I09112 Sequence 9
17	162.6	83.4	600	6 I09105	I09105 Sequence 2
18	162.6	83.4	606	6 I09111	I09111 Sequence 8
19	162.6	83.4	798	6 I09107	I09107 Sequence 4

20	162.6	83.4	810	6 I09109	I09109 Sequence 6
21	162.6	83.4	1469	1 SG148IGG	X04015 Streptococc
22	162.6	83.4	1469	6 A12446	A12446 1.5 kb EcoR
23	162.6	83.4	1576	1 SG148PG	X53324 Streptococc
24	162.6	83.4	1950	1 STRSPGIGP	M13825 Streptococc
25	162.6	83.4	1950	6 I08536	I08536 Sequence 2
26	162.6	83.4	1950	6 I09115	I09115 Sequence 23
27	162.6	83.4	2384	1 SGSPG	Y00428 Streptococc
28	162.6	83.4	2384	6 I08537	I08537 Sequence 4
29	162.6	83.4	2456	1 SGPROTG	X06173 Streptococc
30	161.8	83.0	165	6 A12443	A12443 DNA for Igg
31	158	81.0	398	6 A69078	A69078 Sequence 8
32	158	81.0	1422	6 I44708	I44708 Sequence 16
33	158	81.0	1422	6 I52114	I52114 Sequence 16
34	158	81.0	1683	6 I44709	I44709 Sequence 18
35	158	81.0	1683	6 I52115	I52115 Sequence 18
36	158	81.0	1695	6 I44711	I44711 Sequence 22
37	158	81.0	1695	6 I52117	I52117 Sequence 22
38	158	81.0	1722	6 I44712	I44712 Sequence 24
39	158	81.0	1722	6 I52118	I52118 Sequence 24
40	153.8	78.9	165	6 A12444	A12444 DNA for Igg
41	149	76.4	390	6 I09114	I09114 Sequence 11
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43	133.2	68.3	402	6 I09108	I09108 Sequence 5
44	131	67.2	191	1 S62801	S62801 Streptococc
45	130	66.7	1555	1 STRMAG	L27798 Streptococc

ALIGNMENTS

RESULT 1
AR438294
LOCUS AR438294 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 5 from patent US 6663862.
ACCESSION AR438294
VERSION AR438294.1 GI:42662959
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 5 16-DEC-2003;
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 195; DB 6; Length 195;
Best Local Similarity 100.0%; Pred. No. 7.8e-41;
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 GCTGTTGATGCTGCTACTGACGAGAAAGTCTTCAAAACAATACGCTAACGACAAACGGTGT 120
Db 61 GCTGTTGATGCTGCTACTGACGAGAAAGTCTTCAAAACAATACGCTAACGACAAACGGTGT 120
Qy 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
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Qy 181 CATCACTAAGCTTTGA 195
Db 181 CATCACTAAGCTTTGA 195

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LOCUS AR438293 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 1 from patent US 6663862.
ACCESSION AR438293
VERSION AR438293.1 GI:42662958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 1 16-DEC-2003;
FEATURES Location/Qualifiers
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Best Local Similarity 99.0%; Pred. No. 5.4e-40;
Matches 193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
QY 61 GCTGTTGATGCTGCTACTGCAGCGGAAAGTCTTCAACAATAACGCTAACGACACGGTGTT 120
Db 61 GCTGTTGATGCTGCTACTGCAGAAAAAGTCTTCAACAATAACGCTAACGACACGGTGTT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195
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LOCUS AR438300 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 19 from patent US 6663862.
ACCESSION AR438300
VERSION AR438300.1 GI:42662965
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 19 16-DEC-2003;
FEATURES Location/Qualifiers
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Query Match 98.4%; Score 191.8; DB 6; Length 195;
Best Local Similarity 99.0%; Pred. No. 5.4e-40;
Matches 193; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
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Db 61 GCTGTTGATGCTGCTACTGCAGAAAAAGTCTTCAACAATAACGCTAACGACACGGTGTT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
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RESULT 4
LOCUS AR438301 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6663862.
ACCESSION AR438301
VERSION AR438301.1 GI:42662966
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 21 16-DEC-2003;
FEATURES Location/Qualifiers
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QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
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Db 61 GCTGTTGATGCTGCTACTGCAATTAAGAGTCTTCAACAATAACGCTAACGACACGGTGTT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195
RESULT 5
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DEFINITION Sequence 23 from patent US 6663862.
ACCESSION AR438302
VERSION AR438302.1 GI:42662967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 23 16-DEC-2003;
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Best Local Similarity 98.5%; Pred. No. 1.4e-39;
Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
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Db 181 CATCACTAAGCTTGA 195
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DEFINITION Sequence 21 from patent US 6663862.
ACCESSION AR438301
VERSION AR438301.1 GI:42662966
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 21 16-DEC-2003;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 98.5%; Pred. No. 1.4e-39;
Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
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Db 61 GCTGTTGATGCTGCTACTGCAATTAAGAGTCTTCAACAATAACGCTAACGACACGGTGTT 120
QY 121 GACGGTGAATGGACTTACGACGATCGGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
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QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195
RESULT 5
LOCUS AR438302 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 23 from patent US 6663862.
ACCESSION AR438302
VERSION AR438302.1 GI:42662967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 23 16-DEC-2003;
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Query Match 97.5%; Score 190.2; DB 6; Length 195;
Best Local Similarity 98.5%; Pred. No. 1.4e-39;
Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


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QY 1 ATGACTACTTACAAATTAAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60
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QY 61 GCTGTTGATGCTGCTACTGCGAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTT 120
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QY 181 CATCACTAAGCTTGA 195
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RESULT 6
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LOCUS AR438298 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 15 from patent US 6663862.
ACCESSION AR438298
VERSION AR438298.1 GI:42662963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 15 16-DEC-2003;
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Db 121 GACGGTGAAGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY 181 CATCACTAAGCTTGA 195
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RESULT 7
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DEFINITION Sequence 7 from patent US 6663862.
ACCESSION AR438295
VERSION AR438295.1 GI:42662960
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 7 16-DEC-2003;
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Db 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195

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DEFINITION Sequence 9 from patent US 6663862.
ACCESSION AR438296
VERSION AR438296.1 GI:42662961
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 195)
AUTHORS Hellinga,H.W. and Sloan,D.J.
TITLE Reagents for detection and purification of antibody fragments
JOURNAL Patent: US 6663862-A 9 16-DEC-2003;
FEATURES
    Location/Qualifiers
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            1..195
                /organism="unknown"
                /mol_type="genomic DNA"

ORIGIN

Query Match 95.9%; Score 187; DB 6; Length 195;
Best Local Similarity 97.4%; Pred. No. 9.9e-39;
Matches 190; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60
Db 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGGCGAAACAACACTACTGAA 60

QY 61 GCTGTTGATGCTGCTACTGCGAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTT 120
Db 61 GCTGTTGATGCTGCTACTGCGAATAAAGTCTTCGCGCAATACGCTAACGACAACGGTGTT 120

QY 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY 181 CATCACTAAGCTTGA 195
Db 181 CATCACTAAGCTTGA 195

RESULT 9
AR438297
LOCUS AR438297 195 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 11 from patent US 6663862.
ACCESSION AR438297
VERSION AR438297.1 GI:42662962
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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 195)
AUTHORS    Hellinga,H.W. and Sloan,D.J.
TITLE      Reagents for detection and purification of antibody fragments
JOURNAL    Patent: US 6663862-A 11 16-DEC-2003;
FEATURES   Location/Qualifiers
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            1..195
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ORIGIN
Query Match      95.9%;   Score 187;   DB 6;   Length 195;
Best Local Similarity 97.4%;   Pred. No. 9.9e-39;
Matches 190;   Conservative 0;   Mismatches 5;   Indels 0;   Gaps 0;

QY      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60

QY      61 GCTGTTGATGCTGCTACTGCAGCGGAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 120
Db      61 GCTGTTGATGCTGCTACTGCAGAAAAGTCCTTCAAACAATACGCTGCGGACAACCGGTGTT 120

QY      121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db      121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY      181 CATCACTAAGCTTGA 195
Db      181 CATCACTAAGCTTGA 195

RESULT 10
AR438299
LOCUS      AR438299      195 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 17 from patent US 6663862.
ACCESSION AR438299
VERSION   AR438299.1 GI:42662964
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 195)
AUTHORS   Hellinga,H.W. and Sloan,D.J.
TITLE     Reagents for detection and purification of antibody fragments
JOURNAL   Patent: US 6663862-A 17 16-DEC-2003;
FEATURES  Location/Qualifiers
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Query Match      94.3%;   Score 183.8;   DB 6;   Length 195;
Best Local Similarity 96.4%;   Pred. No. 6.8e-38;
Matches 188;   Conservative 0;   Mismatches 7;   Indels 0;   Gaps 0;

QY      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60

QY      61 GCTGTTGATGCTGCTACTGCAGCGGAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 120
Db      61 GCTGTTGATGCTGCTACTGCAGAAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 120

QY      121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db      121 GACGGTGAATGGCGGCGGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY      181 CATCACTAAGCTTGA 195
Db      181 CATCACTAAGCTTGA 195

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 195)
AUTHORS    Hellinga,H.W. and Sloan,D.J.
TITLE      Reagents for detection and purification of antibody fragments
JOURNAL    Patent: US 6663862-A 17 16-DEC-2003;
FEATURES   Location/Qualifiers
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            /organism="unknown"
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ORIGIN
Query Match      94.3%;   Score 183.8;   DB 6;   Length 195;
Best Local Similarity 96.4%;   Pred. No. 6.8e-38;
Matches 188;   Conservative 0;   Mismatches 7;   Indels 0;   Gaps 0;

QY      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60

QY      61 GCTGTTGATGCTGCTACTGCAGCGGAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 120
Db      61 GCTGTTGATGCTGCTACTGCAGAAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 120

QY      121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180
Db      121 GACGGTGAATGGCGGCGGACGATGCGACTAAGACCTTTACAGTTACTGAACATCACCAT 180

QY      181 CATCACTAAGCTTGA 195
Db      181 CATCACTAAGCTTGA 195
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Db      181 CATCACTAAGCTTGA 195

RESULT 11
AR079001
LOCUS      AR079001      1308 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 4 from patent US 5965390.
ACCESSION AR079001
VERSION   AR079001.1 GI:10005747
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
            1 (bases 1 to 1308)
REFERENCE BJORCK,L. and SJOBROING,U.
TITLE     Protein L and hybrid proteins thereof
JOURNAL   Patent: US 5965390-A 4 12-OCT-1999;
FEATURES  Location/Qualifiers
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            /mol_type="unassigned DNA"

ORIGIN
Query Match      84.0%;   Score 163.8;   DB 6;   Length 1308;
Best Local Similarity 96.0%;   Pred. No. 1.3e-32;
Matches 168;   Conservative 0;   Mismatches 7;   Indels 0;   Gaps 0;

QY      1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db      919 ATGGACACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 978

QY      61 GCTGTTGATGCTGCTACTGCAGCGGAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 120
Db      979 GCTGTTGATGCTGCTACTGCAGAAAAGTCCTTCAAACAATACGCTAACGACAACCGGTGTT 1038

QY      121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 175
Db      1039 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 1093

RESULT 12
S50809
LOCUS      S50809      1365 bp      mRNA      linear      BCT 02-MAR-2001
DEFINITION protein LG=immunoglobulin binding protein {immunoglobulin binding domains} [streptococcus, mRNA Recombinant, 1365 nt].
ACCESSION S50809
VERSION   S50809.1 GI:261705
KEYWORDS
SOURCE    Finnegoldia magna
            Finnegoldia magna
            Bacteria; Firmicutes; Clostridia; Clostridiales;
            Peptostreptococaceae; Finnegoldia.
REFERENCE 1 (bases 1 to 1365)
AUTHORS   Kihlberg,B.M., Sjobring,U., Kastern,W. and BJORCK,L.
TITLE     Protein LG: a hybrid molecule with unique immunoglobulin binding properties
JOURNAL   J. Biol. Chem. 267 (35), 25583-25588 (1992)
MEDLINE   93094283
PUBMED    1460053
REMARK    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsg 120302] from the original journal article.
FEATURES  Location/Qualifiers
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            /organism="Streptococcus sp."
            /mol_type="mRNA"
            /db_xref="taxon:1306"
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/product="protein LG"
/protein_id="AAA03280.1"
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/translation="MKKTAIAIAVALAGFATVAQAAVENKEETPETPETDSEEEVTIK
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DLLAKENGKYTVDVADKGYTLNKFAGKEKTPPEEPKEEVTIKANLIYADGKTQTAEFK
GTFAEATAEAYRYADLLAKENGKYTADLEDGGYTNIRFAGKKVDEKPEEPMDTYKLI
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TVTEM"

ORIGIN

Query Match 84.0%; Score 163.8; DB 1; Length 1365;
Best Local Similarity 96.0%; Pred. No. 1.3e-32;
Matches 168; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGACTACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 60
Db 982 ATGGACACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAA 1041

Qy 61 GCTGTTGATGCTGCTACTGCGAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 120
Db 1042 GCTGTTGATGCTGCTACTGCGAGAAAAGTCTTCAAACAATACGCTAACGACAACGGTGT 1101

Qy 121 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 175
Db 1102 GACGGTGAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACAAAC 1156

RESULT 13

I09113 LOCUS 396 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 10 from Patent WO 8810306.
ACCESSION I09113
VERSION I09113.1 GI:588185
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 396)
AUTHORS Fahnestock,S.R.
TITLE CLONED PROTEIN G VARIANT GENES AND THE PROTEIN G VARIANTS EXPRESSED THEREFROM
JOURNAL Patent: WO 8810306-A 10 29-DEC-1988;
FEATURES Location/Qualifiers
source 1..396
/organism="unknown"
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ORIGIN

Query Match 83.4%; Score 162.6; DB 6; Length 396;
Best Local Similarity 97.6%; Pred. No. 2.6e-32;
Matches 165; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 66
Db 31 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 90

Qy 67 GATGCTGCTACTGCGAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 126
Db 91 GATGCTGCTACTGCGAGAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 150

Qy 127 GAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 175
Db 151 GAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACAAAC 199

RESULT 14

I09106 LOCUS 435 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8810306.
ACCESSION I09106
VERSION I09106.1 GI:588178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 435)
AUTHORS Fahnestock,S.R.
TITLE CLONED PROTEIN G VARIANT GENES AND THE PROTEIN G VARIANTS EXPRESSED THEREFROM
JOURNAL Patent: WO 8810306-A 3 29-DEC-1988;
FEATURES Location/Qualifiers
source 1..435
/organism="unknown"
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ORIGIN

Query Match 83.4%; Score 162.6; DB 6; Length 435;
Best Local Similarity 97.6%; Pred. No. 2.6e-32;
Matches 165; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 66
Db 31 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 90

Qy 67 GATGCTGCTACTGCGAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 126
Db 91 GATGCTGCTACTGCGAGAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 150

Qy 127 GAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 175
Db 151 GAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACAAAC 199

RESULT 15

I09104 LOCUS 447 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 1 from Patent WO 8810306.
ACCESSION I09104
VERSION I09104.1 GI:588176
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 447)
AUTHORS Fahnestock,S.R.
TITLE CLONED PROTEIN G VARIANT GENES AND THE PROTEIN G VARIANTS EXPRESSED THEREFROM
JOURNAL Patent: WO 8810306-A 1 29-DEC-1988;
FEATURES Location/Qualifiers
source 1..447
/organism="unknown"
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ORIGIN

Query Match 83.4%; Score 162.6; DB 6; Length 447;
Best Local Similarity 97.6%; Pred. No. 2.6e-32;
Matches 165; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 66
Db 28 ACTTACAAATTAATCCTTAATGGTAAACATTGAAAGCGGAAACAACACTACTGAAGCTGTT 87

Qy 67 GATGCTGCTACTGCGAGCGAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 126
Db 88 GATGCTGCTACTGCGAGAAAAGTCTTCAAACAATACGCTAACGACAACGGTGTGACGGT 147

Qy 127 GAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACATC 175
Db 148 GAATGGACTTACGACGATGCGACTAAGACCTTTACAGTTACTGAACAAAC 196

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Job time : 1720 secs
